

1644

## RAW SEQUENCE LISTING

DATE: 03/21/2001

PATENT APPLICATION: US/09/609,383

TIME: 14:47:51

Input Set : A:\68030001.app

Output Set: N:\CRF3\03212001\I609383.raw

P.5

3 <110> APPLICANT: HEINEGARD, DICK  
4 LORENZO, PILAR  
6 <120> TITLE OF INVENTION: CARTILAGE INTERMEDIATE LAYER PROTEIN AND NUCLEIC ACIDS  
7 THEREFOR  
9 <130> FILE REFERENCE: 02386.0046 SEQUENCE LISTING  
11 <140> CURRENT APPLICATION NUMBER: 09/609,383  
12 <141> CURRENT FILING DATE: 2000-07-03  
14 <150> PRIOR APPLICATION NUMBER: 60/142,054  
15 <151> PRIOR FILING DATE: 1999-07-02  
17 <160> NUMBER OF SEQ ID NOS: 22  
19 <170> SOFTWARE: PatentIn Ver. 2.1  
21 <210> SEQ ID NO: 1  
22 <211> LENGTH: 4175  
23 <212> TYPE: DNA  
24 <213> ORGANISM: Homo sapiens  
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**ENTERED  
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MAR 29 2001

TECH CENTER 1600/2900

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99 &lt;210&gt; SEQ ID NO: 2

100 &lt;211&gt; LENGTH: 1184

101 &lt;212&gt; TYPE: PRT

102 &lt;213&gt; ORGANISM: Homo sapiens

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106 1 5 10 15

108 Thr Ser Val Leu Gly Arg Gln Thr Met Leu Thr Gln Ser Val Arg Arg

109 20 25 30

111 Val Gln Pro Gly Lys Lys Asn Pro Ser Ile Phe Ala Lys Pro Ala Asp

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118 65          70          75          80
120 Tyr Gly Asp Arg Val Cys Ala Arg Pro Leu Arg Leu Glu Ala Arg Thr
121          85          90          95
123 Thr Asp Trp Thr Pro Ala Gly Ser Thr Gly Gln Val Val His Gly Ser
124          100          105          110
126 Pro Arg Glu Gly Phe Trp Cys Leu Asn Arg Glu Gln Arg Pro Gly Gln
127          115          120          125
129 Asn Cys Ser Asn Tyr Thr Val Arg Phe Leu Cys Pro Pro Gly Ser Leu
130          130          135          140
132 Arg Arg Asp Thr Glu Arg Ile Trp Ser Pro Trp Ser Pro Trp Ser Lys
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135 Cys Ser Ala Ala Cys Gly Gln Thr Gly Val Gln Thr Arg Thr Arg Ile
136          165          170          175
138 Cys Leu Ala Glu Met Val Ser Leu Cys Ser Glu Ala Ser Glu Glu Gly
139          180          185          190
141 Gln His Cys Met Gly Gln Asp Cys Thr Ala Cys Asp Leu Thr Cys Pro
142          195          200          205
144 Met Gly Gln Val Asn Ala Asp Cys Asp Ala Cys Met Cys Gln Asp Phe
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147 Met Leu His Gly Ala Val Ser Leu Pro Gly Gly Ala Pro Ala Ser Gly
148 225          230          235          240
150 Ala Ala Ile Tyr Leu Leu Thr Lys Thr Pro Lys Leu Leu Thr Gln Thr
151          245          250          255
153 Asp Ser Asp Gly Arg Phe Arg Ile Pro Gly Leu Cys Pro Asp Gly Lys
154          260          265          270
156 Ser Ile Leu Lys Ile Thr Lys Val Lys Phe Ala Pro Ile Val Leu Thr
157          275          280          285
159 Met Pro Lys Thr Ser Leu Lys Ala Ala Thr Ile Lys Ala Glu Phe Val
160          290          295          300
162 Arg Ala Glu Thr Pro Tyr Met Val Met Asn Pro Glu Thr Lys Ala Arg
163 305          310          315          320
165 Arg Ala Gly Gln Ser Val Ser Leu Cys Cys Lys Ala Thr Gly Lys Pro
166          325          330          335
168 Arg Pro Asp Lys Tyr Phe Trp Tyr His Asn Asp Thr Leu Leu Asp Pro
169          340          345          350
171 Ser Leu Tyr Lys His Glu Ser Lys Leu Val Leu Arg Lys Leu Gln Gln
172          355          360          365
174 His Gln Ala Gly Glu Tyr Phe Cys Lys Ala Gln Ser Asp Ala Gly Ala
175          370          375          380
177 Val Lys Ser Lys Val Ala Gln Leu Ile Val Thr Ala Ser Asp Glu Thr
178 385          390          395          400
180 Pro Cys Asn Pro Val Pro Glu Ser Tyr Leu Ile Arg Leu Pro His Asp
181          405          410          415
183 Cys Phe Gln Asn Ala Thr Asn Ser Phe Tyr Tyr Asp Val Gly Arg Cys
184          420          425          430

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189 Asp Ala Val Gln Asn Cys Cys Gly Ile Ser Lys Thr Glu Glu Arg Glu
190           450           455           460
192 Ile Gln Cys Ser Gly Tyr Thr Leu Pro Thr Lys Val Ala Lys Glu Cys
193 465           470           475           480
195 Ser Cys Gln Arg Cys Thr Glu Thr Arg Ser Ile Val Arg Gly Arg Val
196           485           490           495
198 Ser Ala Ala Asp Asn Gly Glu Pro Met Arg Phe Gly His Val Tyr Met
199           500           505           510
201 Gly Asn Ser Arg Val Ser Met Thr Gly Tyr Lys Gly Thr Phe Thr Leu
202           515           520           525
204 His Val Pro Gln Asp Thr Glu Arg Leu Val Leu Thr Phe Val Asp Arg
205           530           535           540
207 Leu Gln Lys Phe Val Asn Thr Thr Lys Val Leu Pro Phe Asn Lys Lys
208 545           550           555           560
210 Gly Ser Ala Val Phe His Glu Ile Lys Met Leu Arg Arg Lys Glu Pro
211           565           570           575
213 Ile Thr Leu Glu Ala Met Glu Thr Asn Ile Ile Pro Leu Gly Glu Val
214           580           585           590
216 Val Gly Glu Asp Pro Met Ala Glu Leu Glu Ile Pro Ser Arg Ser Phe
217           595           600           605
219 Tyr Arg Gln Asn Gly Glu Pro Tyr Ile Gly Lys Val Lys Ala Ser Val
220           610           615           620
222 Thr Phe Leu Asp Pro Arg Asn Ile Ser Thr Ala Thr Ala Ala Gln Thr
223 625           630           635           640
225 Asp Leu Asn Phe Ile Asn Asp Glu Gly Asp Thr Phe Pro Leu Arg Thr
226           645           650           655
228 Tyr Gly Met Phe Ser Val Asp Phe Arg Asp Glu Val Thr Ser Glu Pro
229           660           665           670
231 Leu Asn Ala Gly Lys Val Lys Val His Leu Asp Ser Thr Gln Val Lys
232           675           680           685
234 Met Pro Glu His Ile Ser Thr Val Lys Leu Trp Ser Leu Asn Pro Asp
235           690           695           700
237 Thr Gly Leu Trp Glu Glu Glu Gly Asp Phe Lys Phe Glu Asn Gln Arg
238 705           710           715           720
240 Arg Asn Lys Arg Glu Asp Arg Thr Phe Leu Val Gly Asn Leu Glu Ile
241           725           730           735
243 Arg Glu Arg Arg Leu Phe Asn Leu Asp Val Pro Glu Ser Arg Arg Cys
244           740           745           750
246 Phe Val Lys Val Arg Ala Tyr Arg Ser Glu Arg Phe Leu Pro Ser Glu
247           755           760           765
249 Gln Ile Gln Gly Val Val Ile Ser Val Ile Asn Leu Glu Pro Arg Thr
250           770           775           780
252 Gly Phe Leu Ser Asn Pro Arg Ala Trp Gly Arg Phe Asp Ser Val Ile
253 785           790           795           800
255 Thr Gly Pro Asn Gly Ala Cys Val Pro Ala Phe Cys Asp Asp Gln Ser
256           805           810           815
258 Pro Asp Ala Tyr Ser Ala Tyr Val Leu Ala Ser Leu Ala Gly Glu Glu

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261 Leu Gln Ala Val Glu Ser Ser Pro Lys Phe Asn Pro Asn Ala Ile Gly
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265          850          855          860
267 Glu Asp Pro Arg Val Lys Lys Thr Ala Phe Gln Ile Ser Met Ala Lys
268 865          870          875          880
270 Pro Arg Pro Asn Ser Ala Glu Glu Ser Asn Gly Pro Ile Tyr Ala Phe
271          885          890          895
273 Glu Asn Leu Arg Ala Cys Glu Glu Ala Pro Pro Ser Ala Ala His Phe
274          900          905          910
276 Arg Phe Tyr Gln Ile Glu Gly Asp Arg Tyr Asp Tyr Asn Thr Val Pro
277          915          920          925
279 Phe Asn Glu Asp Asp Pro Met Ser Trp Thr Glu Asp Tyr Leu Ala Trp
280          930          935          940
282 Trp Pro Lys Pro Met Glu Phe Arg Ala Cys Tyr Ile Lys Val Lys Ile
283 945          950          955          960
285 Val Gly Pro Leu Glu Val Asn Val Arg Ser Arg Asn Met Gly Gly Thr
286          965          970          975
288 His Arg Arg Thr Val Gly Lys Leu Tyr Gly Ile Arg Asp Val Arg Ser
289          980          985          990
291 Thr Arg Asp Arg Asp Gln Pro Asn Val Ser Ala Ala Cys Leu Glu Phe
292          995          1000          1005
294 Lys Cys Ser Gly Met Leu Tyr Asp Gln Asp Arg Val Asp Arg Thr Leu
295          1010          1015          1020
297 Val Lys Val Ile Pro Gln Gly Ser Cys Arg Arg Ala Ser Val Asn Pro
298 1025          1030          1035          1040
300 Met Leu His Glu Tyr Leu Val Asn His Leu Pro Leu Ala Val Asn Asn
301          1045          1050          1055
303 Asp Thr Ser Glu Tyr Thr Met Leu Ala Pro Leu Asp Pro Leu Gly His
304          1060          1065          1070
306 Asn Tyr Gly Ile Tyr Thr Val Thr Asp Gln Asp Pro Arg Thr Ala Lys
307          1075          1080          1085
309 Glu Ile Ala Leu Gly Arg Cys Phe Asp Gly Thr Ser Asp Gly Ser Ser
310          1090          1095          1100
312 Arg Ile Met Lys Ser Asn Val Gly Val Ala Leu Thr Phe Asn Cys Val
313 1105          1110          1115          1120
315 Glu Arg Gln Val Gly Arg Gln Ser Ala Phe Gln Tyr Leu Gln Ser Thr
316          1125          1130          1135
318 Pro Ala Gln Ser Pro Ala Ala Gly Thr Val Gln Gly Arg Val Pro Ser
319          1140          1145          1150
321 Arg Arg Gln Gln Arg Ala Ser Arg Gly Gly Gln Arg Gln Ser Gly Val
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331 <210> SEQ ID NO: 3
332 <211> LENGTH: 18
333 <212> TYPE: PRT
334 <213> ORGANISM: Homo sapiens

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FYI:

**Please Note:**

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY  
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L:358 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4  
L:393 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7  
L:421 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9  
L:449 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11  
L:527 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18  
L:555 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20